

## Sequence Listing

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               ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=  
 30     Methylobacter; ZF0051321= Bacterium; ZF0050782= Lactobacillus  
               bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=  
               Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=  
               Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=  
               Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=  
               Streptomyces; ZF0002437= Streptomyces; ZF0003712=  
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               ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=  
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 35 40 45  
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35 Thr Ile Ala Thr Pro Leu Thr Leu Gly His Glu Phe Val Gly Glu Val  
20 25 30

40 Val Glu Thr Gly Arg Asp Val Thr Asp Ile Gln Val Gly Asp Leu Val  
35 40 45

45 Ser Gly Glu Gly His Leu Val Cys Gly Lys Cys Arg Asn Cys Leu Ala  
50 55 60

50 Gly Arg Arg His Leu Cys Arg Ala Thr Val Gly Leu Gly Val Gly Arg  
65 70 75 80

55 Asp Gly Ala Phe Ala Glu Tyr Val Val Leu Pro Ala Ser Asn Val Trp  
85 90 95

Val His Arg Val Pro Val Asp Leu Asp Val Ala Ala Ile Phe Asp Pro  
100 105 110

Phe Gly Asn Ala Val His Thr Ala Leu Ser Phe Pro Leu Val Gly Glu

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	130	135	140
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	<213> unknown		
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15	<221> source		
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	ZF0050330= Bacillus, ZF0002852= Rhodococcus; ZF0050310=		
20	Arthrobacter paraffineus; ZF0002437= Streptomyces; ZF0003712=		
	Micromonospora; ZF0003765= Streptomyces; ZF0002332=		
	Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;		
	ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;		
	ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=		
25	Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;		
	ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=		
	Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes		
	nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=		
	Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;		
30	ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=		
	Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;		
	ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;		
	ZF0003528= Actinomyces; ZF0003529= Actinomyces;		
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40	Ser Ala Val Thr Gly Tyr Arg Glu Gly Gln Arg Val Ile Ala Gly Ala		
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45	Ile Cys Pro Asn Phe Asn Ser Tyr Ala Ala Gln Asp Gly Ala Pro Ser		
	35 40 45		
50	Gln Asp Gly Ser Tyr Leu Val Ala Ser Gly Ala Cys Gly Cys His Gly		
	50 55 60		
55	Tyr Arg Ala Thr Ala Gly Trp Arg Phe Gly Asn Ile Ile Asp Gly Ala		
	65 70 75 80		
	Gln Ala Glu Tyr Leu Leu Val Pro Asp Ala Gln Gly Asn Leu Ala Pro		
	85 90 95		

16

Val Pro Asp Asn Leu Ser Asp Glu Gln Val Leu Met Cys Pro Asp Ile  
 100 105 110

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Met Ser Thr Gly Phe Lys Gly Ala Glu Asn Ala His Ile Arg Ile Gly  
 115 120 125

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Asp Thr Val Ala Val Phe Ala Gln Gly Pro  
 130 135

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<210> 17  
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 Micromonospora; ZF0003765= Streptomyces; ZF0002332=  
 Streptomyces diatsatochromogenes; ZF0003768= Actinomyces;  
 ZF0002379= Streptomyces coelestis; ZF0002443= Streptomyces;  
 ZF0002442= Streptomyces; ZF0002436= Streptomyces; ZF0050994=  
 Bacterium; ZF0050992= Bacterium; ZF0050442= Bacterium;  
 ZF0002049= Streptomyces; ZF0006069= Streptomyces; ZF0006075=  
 Streptomyces; ZF0004724= Nocardiaform; ZF0002392= Actinoplanes  
 nipponensis; ZF0002356= Actinoplanes brasiliensis; ZF0003501=  
 Actinomyces; ZF0051322= Bacterium; ZF0006078= Streptomyces;  
 ZF0006092= Streptomyces; ZF0006090= Streptomyces; ZF0006084=  
 Streptomyces; ZF0006068= Streptomyces; ZF0050284= Rhodococcus;  
 ZF0050028= Agrobacterium tumefaciens; ZF0003540= Actinomyces;  
 ZF0003528= Actinomyces; ZF0003529= Actinomyces;

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35

40

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45

Cys Gly Thr Asp Leu His Ile Leu Gly Gly Asp Val Pro Glu Val Thr  
 1 5 10 15

50

Asp Gly Arg Ile Leu Gly His Glu Ala Val Gly Thr Val Val Glu Val  
 20 25 30

Gly Asp Gly Val Gln Thr Leu Ala Pro Gly Asp Arg Val Leu Val Ser  
 35 40 45

55

Cys Val Thr Ala Cys Gly Thr Cys Arg Phe Cys Arg Glu Ser Arg Tyr  
 50 55 60



Gly Gln Cys Leu Gly Gly Gly Gly Trp Ile Leu Gly His Leu Ile Asp  
 65 70 75 80

5 Gly Thr Gln Ala Glu Leu Val Arg Val Pro Tyr Ala Asp Asn Ser Thr  
 85 90 95

10 His Arg Ile Pro Asp Gly Val Ser Asp Glu Gln Met Leu Met Leu Ala  
 100 105 110

15 Asp Ile Leu Pro Thr Ser Tyr Glu Val Gly Val Leu Asn Gly Cys Leu  
 115 120 125

20 Arg Pro Ala Asp Val Val Val Ile Ile Gly Ala Asp Asp Arg Pro Leu  
 130 135 140

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25 <211> 73  
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 <213> unknown

30 <220>  
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 <223> ZF0050310= *Arthrobacter paraffineus*

35 <400> 18

Val Asp Val Val Val Asp Asn Ala Gly Phe Gly Thr His Gly Ala Phe  
 1 5 10 15

40 Val Asp Glu Asp His Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile  
 20 25 30

45 Ala Thr Leu Val Glu Leu Thr His Thr Phe Pro Pro Asp Leu Leu Thr  
 35 40 45

Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro  
 50 55 60

5 Thr Pro Gly Met Ala Val Tyr Cys Ala  
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10 <210> 19  
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 <212> PRT

15 <213> unknown  
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20 <221> source  
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25 Val Asp Val Val Val His Asn Ala Gly Phe Gly Thr His Gly Ala Phe  
 1 5 10 15

30 Val Asp Glu Asp Leu Glu Arg Val Thr Ser Glu Ile Gln Leu Asn Ile  
 20 25 30

35 Ala Thr Leu Val Glu Leu Thr His Thr Phe Leu Pro Asp Leu Leu Thr  
 35 40 45

40 Gly Arg Gly Ala Leu Val Asn Ile Ala Ser Thr Ala Ser Phe Gln Pro  
 50 55 60

45 Thr Pro Gly Met Ala Val Tyr Cys Ala Thr Lys  
 65 70 75

50 <210> 20  
 <211> 79  
 <212> PRT

55 <213> unknown  
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<212> PRT

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<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

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15

Thr Val Ala Ile Gly Asp Ile Asp Glu Ala Thr Leu Ala Arg Ala Ala  
20 25 30

20

Lys Asp Leu Gly Ile Arg Thr Phe Gly Arg Leu Asp Val Thr Asp Pro  
35 40 45

25

Ala Ser Phe Phe Asp Phe Leu Asp Thr Val Glu Gly Glu Leu Gly Pro  
50 55 60

30

Ile Asp Val Leu Ile Asn Asn Ala  
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<210> 23

35 <211> 75

<212> PRT

<213> unknown

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<220>

<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

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<400> 23

Gln Arg Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala  
1 5 10 15

50

Thr Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val  
20 25 30

55

Ala Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val  
35 40 45

Arg Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala  
 50 55 60

5 Phe Gly Pro Val Asp Val Met Met Asn Asn Ala  
 65 70 75

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 <211> 72  
 <212> PRT

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 20 <223> ZF0050310= *Arthrobacter paraffineus*  
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25 Gln Gly Ile Gly Tyr Gln Thr Ala Lys Glu Leu Ile Arg Arg Gly His  
 1 5 10 15

30 Arg Val Ala Ile Gly Asp Ile Asp Glu Ala Arg Ala Lys Glu Thr Ala  
 20 25 30

35 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Asp Pro  
 35 40 45

40 Asp Ser Phe Lys Asp Phe Leu Asp Leu Val Glu Gly Asp Leu Gly Pro  
 50 55 60

45 Leu Asp Val Leu Ile Asn Asn Ala  
 65 70

50 <210> 25  
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Gly Ile Gly Leu Glu Ile Ala Arg Thr Phe Ile Lys Glu Gly Ala Thr  
 1 5 10 15  
 5 Val Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Ala  
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 10 Glu Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg  
 35 40 45  
 Asp Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe  
 50 55 60  
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 Gly Pro Val Asp Val Ile Val Asn Asn Ala  
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 <211> 74  
 25  
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 40 Val Leu Gly Asp Ile Asn Glu Thr Val Gly Thr Ala Ala Val Gly Glu  
 20 25 30  
 45 Leu Gly Gly Glu Ser Val Ala Arg Phe Ala Ser Cys Asp Val Arg Asp  
 35 40 45  
 50 Ser Gly Gln Val Glu Ala Met Leu Asp Leu Ala Glu Ser Ala Phe Gly  
 50 55 60  
 55 Pro Val Asp Val Met Val Asn Asn Ala Gly  
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 <211> 62

<212> PRT  
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 5 <220>  
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 1 5 10 15  
 15  
 Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala Leu Ala Leu Glu  
 20 20 25 30  
 Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala Phe Glu Ala Thr  
 35 40 45  
 25 Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn Asn Ala  
 50 55 60  
 30 <210> 28  
 <211> 74  
 <212> PRT  
 35 <213> unknown  
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 40 <221> source  
 <223> ZF0002333= Rhodococcus erythropolis  
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 Val Val Asn Asp Leu Asp Pro Glu Pro Ala Ala Gln Thr Glu Arg Asp  
 50 20 25 30  
 Ile Lys Ala Thr Gly Gly Gln Ala Val Ser Cys Val Gly Ser Val Ala  
 55 35 40 45  
 Glu Asp Gly Phe Ala Glu Arg Phe Val Asn Thr Ala Val Glu Ser Phe  
 50 55 60

Gly Gly Leu Asp Val Met Val Asn Asn Ala  
 65 70

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 <210> 29  
 <211> 76

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 <212> PRT  
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15  
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 <400> 29

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 Ala Gly Leu Gly Val Glu Phe Ala His Arg Phe Ala Ala Arg Gly Ala  
 1 5 10 15

25  
 Asn Leu Val Leu Val Ala Arg Arg Ala Asp Arg Leu Glu Ala Leu Ala  
 20 25 30

30  
 Thr Glu Leu Arg Val Ala His Gly Ile Thr Val Thr Val Leu Pro Ala  
 35 40 45

35  
 Asp Leu Ala Ala Pro Gly Val Gly Ala Thr Leu His Gln Glu Leu Thr  
 50 55 60

40  
 Ser Arg Gly Ile Thr Val Thr Ser Leu Ile Asn Asn  
 65 70 75

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 <213> unknown  
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 1 5 10 15



Arg Val Ala Ile Val Asp Ile Asp Glu Ala Arg Ala Lys Gly Ala Ala  
 20 25 30

5 Ala Glu Leu Gly Val Lys Val Val Thr Arg Leu Asp Val Thr Glu Pro  
 35 40 45

10 Asp Ser Phe Thr Thr Phe Leu Asp Leu Val Glu Arg Glu Leu Gly Pro  
 50 55 60

15 Leu Asp Ile Leu Val Asn Asn Ala  
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<210> 31

20 <211> 67

<212> PRT

<213> unknown

25 <220>

<221> source

<223> ZF0050310= *Arthrobacter paraffineus*

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 1 5 10 15

35 Ala Glu Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala  
 20 25 30

40 Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala  
 35 40 45

45 Phe Glu Ala Thr Val Ala Glu Trp Gly Arg Phe Asp Tyr Leu Val Asn  
 50 55 60

50 Asn Ala Gly  
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<210> 32

<211> 67

55 <212> PRT

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 5 <400> 32  
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 1 5 10 15  
 Ala Lys Glu Thr Val Ala Leu Ile Glu Ser Gln Tyr Gly Thr Pro Ala  
 20 25 30  
 15 Leu Ala Leu Glu Ala Asp Val Arg Asp Arg Ala Ala Val Ser Ala Ala  
 35 40 45  
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 50 55 60  
 20 Asn Ala Gly  
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 25 <210> 33  
 <211> 348  
 30 <212> PRT  
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 35 <221> source  
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 1 5 10 15  
 45 Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val  
 20 25 30  
 Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro  
 50 35 40 45  
 Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly  
 50 55 60  
 55 Ala Gly Arg Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile  
 65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Ser Cys Trp  
 85 90 95

5 His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Lys Glu Leu  
 100 105 110

10 Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe  
 115 120 125

15 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp  
 130 135 140

20 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His  
 145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ala Tyr Ala Val  
 165 170 175

25 Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg  
 180 185 190

30 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys  
 195 200 205

35 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp  
 210 215 220

40 Lys Asp Ala Ala Glu Asn Val Arg Arg Ile Thr Gly Ser Gln Gly Ala  
 225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala  
 245 250 255

45 Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly  
 260 265 270

50 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu  
 275 280 285

55 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
 290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ala Val Glu Thr  
 305 310 315 320

	Phe	Ser	Leu	Asp	Asn	Gly	Ala	Glu	Ala	Tyr	Arg	Arg	Leu	Ala	Ala	Gly	
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5																	
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	Glu	Ile	Pro	Lys	Pro	Glu	Pro	Gly	Pro	Gly	Glu	Val	Leu	Leu	Glu	Val	
30				20					25					30			
	Thr	Ala	Ala	Gly	Val	Cys	His	Ser	Asp	Asp	Phe	Ile	Met	Ser	Leu	Pro	
35			35					40					45				
	Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
	50						55					60					
40																	
	Ala	Gly	Arg	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
	65					70					75					80	
45	Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Ser	Cys	Trp	
					85					90					95		
	His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Lys	Glu	Leu	
50				100					105					110			

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe  
 115 120 125

5 Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp  
 130 135 140

10 Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His  
 145 150 155 160

15 Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ala Tyr Ala Val  
 165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg  
 180 185 190

20 His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys  
 195 200 205

25 Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp  
 210 215 220

30 Lys Asp Ala Ala Glu Asn Val Arg Arg Ile Thr Gly Ser Gln Gly Ala  
 225 230 235 240

35 Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala  
 245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly  
 260 265 270

40 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu  
 275 280 285

45 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu  
 290 295 300

50 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ala Val Glu Thr  
 305 310 315 320

55 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly  
 325 330 335

Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu  
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 ZF0050330= Bacillus; ZF0051303= Bacterium; ZF0051337=  
 Methylobacter; ZF0051321= Bacterium; ZF0050782= Lactobacillus  
 bulgaricus; ZF0050544= Phyllobacterium rubiacearum; ZF0002852=  
 Rhodococcus; ZF0050310= Arthrobacter paraffineus; ZF0002862=  
 20 Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0002031=  
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=  
 Streptomyces; ZF0002437= Streptomyces; ZF0003712=  
 Micromonospora; ZF0003765= Streptomyces; ZF0051305= Bacterium;  
 ZF0003513= Actinomyces; ZF0050993= Kocuria; ZF0002018=  
 25 Streptomyces; ZF0003767= Actinomyces; ZF0002332= Streptomyces  
 diastatochromogenes; ZF0003768= Actinomyces; ZF0002379=  
 Streptomyces coelestis; ZF0002351= Nonomuraea roseoviolacea;  
 ZF0003769= Actinomyces;  
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 35 ttcatgatcg tcgattctcc tcgccacett gtcccgatcg gtgacctga cccggtcaag  
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 40 240  
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 45 attcagctcc tccgtcacct ctggcgctca acggtcatcg ctttggacgt gagcgccgac  
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 aagctcgaac tggcaaccaa ggtaggcgct cacgaagtgg ttctgtccga caaggacgag  
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 ZF0050330= *Bacillus*; ZF0051303= *Bacterium*; ZF0051337=  
 15 *Methylobacter*; ZF0051321= *Bacterium*; ZF0050782= *Lactobacillus*  
*bulgaricus*; ZF0050544= *Phyllobacterium rubiacearum*; ZF0002852=  
*Rhodococcus*; ZF0050310= *Arthrobacter paraffineus*; ZF0002862=  
*Streptomyces clavuligerus*; ZF0050292= *Bacterium*; ZF0002031=  
*Streptomyces*; ZF0002349= *Streptomyces spectabilis*; ZF0002434=  
*Streptomyces*; ZF0002437= *Streptomyces*; ZF0003712=  
 20 *Micromonospora*; ZF0003765= *Streptomyces*; ZF0051305= *Bacterium*;  
 ZF0003513= *Actinomyces*; ZF0050993= *Kocuria*; ZF0002018=  
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*diastatochromogenes*; ZF0003768= *Actinomyces*; ZF0002379=  
*Streptomyces coelestis*; ZF0002351= *Nonomuraea roseoviolacea*;  
 ZF0003769= *Actinomyces*;  
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 30 120  
 ttcatgatcg tcgattctcc tcgccacctt gtcccgatcg gtgacctcga cccggtcaag  
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 35 acggtgcccgc tgaccgacgc cggctctgacg ccgtatcacg cgatcaagcg ttctctgccg  
 240  
 aaacttcgcg gaggctcgta cgcggttgtc attggtaccg gcgggctcgg ccacgtcacc  
 300  
 40 attcagctcc tccgtcacct ctcgccggca acggtcatcg ctttggacgt gagcgccgac  
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 <210> 37  
 50 <211> 486  
 <212> DNA  
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 55 <220>  
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 <223> ZF0050286= *Corynebacterium hoagii*

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120  
tacatgatcg tcgactcgcc gcgtcacctg gtcccgatcg gtgacctga ccccgtcacg  
10 180  
acgggtgccgc tgaccgacgc cgggctcacc cgtaccacg cgatcaaacg gtcgctcggc  
240  
15 aagctccgcg ccggctcgta cgcagtcgtg atcggcaccg gaggcctcgg acacgtcggc  
300  
atccagctgc tccgccacct gtcccctgca cgcattcatcg ccctcgacgt caacgacgag  
20 360  
aagctcgcgt tcgcccgcga ggtcggcgcg caccgagaccg tgttgtcgaa cgccgacgcc  
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25 gccgcgaacg tccggaagat caccgggttcg gccgggtgccg cgctgggtcct agacttcgtc  
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486  
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<210> 38  
<211> 483  
35 <212> DNA  
<213> unknown  
<220>  
40  
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<223> ZF0050310= *Arthrobacter paraffineus*  
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50 120  
ttcatgatcg tcgattcacc tcgccacctc gtcccgatcg gcgacctga tccgggtcaag  
180  
acgggtgccac tgaccgacgc cgggtctgact ccgtatcacg cgatcaagcg ttactgccc  
55 240  
aaacttcgcg gtggcgcgta cgccgtcgtc atcggtaccg gcggtctcgg ccatgtcgcc  
300



atccaactcc tccgccacct ctcggcagca accgtcatcg cactcgacgt gagcgcgagc  
 360  
 aagctcgtac tggcaaccaa ggtaggcgct cacgaagtgg tcctgtccga caaggacgcg  
 5 420  
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 1.0 ggc  
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 15 <211> 210  
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 20 <213> unknown  
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 ZF0003868= Actinomadura; ZF0004213= Actinomyces; ZF0003876=  
 Actinomyces; ZF0003866= Actinomyces; ZF0003864= Actinomyces;  
 ZF0003862= Actinomadura; ZF0003869= Actinomyces; ZF0003867=  
 30 Actinomadura; ZF0004216= Actinomyces; ZF0004235= Actinomyces;  
 ZF0004209= Actinomadura; ZF0004214= Actinomyces; ZF0003871=  
 Actinomyces; ZF0004063= Actinomadura; ZF0004052= Actinomadura;  
 ZF0006405= Streptomyces; ZF0003865= Actinomadura; ZF0004047=  
 Actinomadura; ZF0004070= Actinomyces; ZF0004085= Actinomyces;  
 35 ZF0004217= Actinomyces; ZF0004089= Actinomadura; ZF0004090=  
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 ZF0051203= Bacterium;  
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 120  
 45 tacatgatcg tcgacgaccc gcgccacctg gtgccgctcg gcggtctcga cccgggtccag  
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 50 210  
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 55 <211> 282  
 <212> DNA  
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<220>

5 <221> source

<223> ZF0002326= Actinoplanes missouriensis; ZF0003505= Streptomyces;  
 ZF0051321= Bacterium; ZF0050782= Lactobacillus bulgaricus;  
 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=  
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=  
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;  
 10 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=  
 Actinoplanes philippinensis; ZF0002441= Streptomyces;  
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=  
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=  
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=  
 15 Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396=  
 Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces;  
 ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087=  
 Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium;  
 ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538=  
 20 Actinomyces; ZF0003535= Actinomyces;

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 120

30 gtcggcgacc acgtcggttct gtccttcatt cgggcttggt gaacctgtcc ggcgtgttcg  
 180

gccggggcatc agaattctttg tgacctcggg atgggcctcc tcagcggcca agccatcagc  
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40 <211> 276

<212> DNA

45 <213> unknown

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50 <221> source

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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031=  
 Streptomyces; ZF0002349= Streptomyces spectabilis; ZF0002434=  
 Streptomyces; ZF0050993= Kocuria; ZF0002018= Streptomyces;  
 55 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331=  
 Actinoplanes philippinensis; ZF0002441= Streptomyces;  
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240=  
 Bacterium; ZF0002333= Rhodococcus erythropolis; ZF0003713=  
 Micromonospora; ZF0004980= Streptomyces; ZF0004821=

Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces; ZF0003535= Actinomyces;

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15 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc  
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ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgccaca ggtcgacggg  
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<210> 42

25 <211> 276

<212> DNA

<213> unknown

30 <220>

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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031= Streptomyces;  
 ZF0002349= Streptomyces spectabilis; ZF0002434= Streptomyces;  
 ZF0050993= Kocuria; ZF0002018= Streptomyces;  
 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331= Actinoplanes philippinensis; ZF0002441= Streptomyces;  
 40 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240= Bacterium;  
 ZF0002333= Rhodococcus erythropolis; ZF0003713= Micromonospora;  
 ZF0004980= Streptomyces; ZF0004821= Actinomyces;  
 45 ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes;  
 ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces;  
 ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium;  
 ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus;  
 ZF0003538= Actinomyces; ZF0003535= Actinomyces;

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ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc  
 180

ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg  
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5 acgtaccgcg cgacagctcg cgggcacgac gtcgga  
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 ZF0050544= Phyllobacterium rubiacearum; ZF0002031= Streptomyces;  
 ZF0002349= Streptomyces spectabilis; ZF0002434= Streptomyces;  
 ZF0050993= Kocuria; ZF0002018= Streptomyces;  
 25 ZF0003767= Actinomyces; ZF0003764= Streptomyces; ZF0002331= Actinoplanes philippinensis; ZF0002441= Streptomyces;  
 ZF0051307= Bacterium; ZF0051301= Bacterium; ZF0051240= Bacterium;  
 ZF0002333= Rhodococcus erythropolis; ZF0003713= Micromonospora;  
 30 ZF0004980= Streptomyces; ZF0004821= Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes;  
 ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces;  
 ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium;  
 35 ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces;  
 ZF0003535= Actinomyces;

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45 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc  
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ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg  
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50 acgtaccgcg cgacagctcg cgggcacgac gtcgga  
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ZF0050544= *Phyllobacterium rubiacearum*; ZF0002031=  
Streptomyces; ZF0002349= *Streptomyces spectabilis*; ZF0002434=  
Streptomyces; ZF0050993= *Kocuria*; ZF0002018= *Streptomyces*;  
10 ZF0003767= *Actinomyces*; ZF0003764= *Streptomyces*; ZF0002331=  
*Actinoplanes philippinensis*; ZF0002441= *Streptomyces*;  
ZF0051307= *Bacterium*; ZF0051301= *Bacterium*; ZF0051240=  
Bacterium; ZF0002333= *Rhodococcus erythropolis*; ZF0003713=  
Micromonospora; ZF0004980= *Streptomyces*; ZF0004821=  
15 Actinomyces; ZF0002359= *Actinoplanes ianthinogenes*; ZF0002396=  
*Actinoplanes*; ZF0003781= *Actinomyces*; ZF0003512= *Actinomyces*;  
ZF0006093= *Streptomyces*; ZF0006103= *Streptomyces*; ZF0006087=  
Streptomyces; ZF0050446= *Bacterium*; ZF0050445= *Bacterium*;  
ZF0006086= *Streptomyces*; ZF0002322= *Rhodococcus*; ZF0003538=  
20 Actinomyces; ZF0003535= *Actinomyces*;

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120  
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30 180  
ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacacg ggtcgacggg  
240  
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<210> 45

40 <211> 276

<212> DNA

45 <213> unknown

<220>

<221> source

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ZF0051321= *Bacterium*; ZF0050782= *Lactobacillus bulgaricus*;  
ZF0050544= *Phyllobacterium rubiacearum*; ZF0002031=  
Streptomyces; ZF0002349= *Streptomyces spectabilis*; ZF0002434=  
Streptomyces; ZF0050993= *Kocuria*; ZF0002018= *Streptomyces*;  
55 ZF0003767= *Actinomyces*; ZF0003764= *Streptomyces*; ZF0002331=  
*Actinoplanes philippinensis*; ZF0002441= *Streptomyces*;  
ZF0051307= *Bacterium*; ZF0051301= *Bacterium*; ZF0051240=  
Bacterium; ZF0002333= *Rhodococcus erythropolis*; ZF0003713=  
Micromonospora; ZF0004980= *Streptomyces*; ZF0004821=

Actinomyces; ZF0002359= Actinoplanes ianthinogenes; ZF0002396= Actinoplanes; ZF0003781= Actinomyces; ZF0003512= Actinomyces; ZF0006093= Streptomyces; ZF0006103= Streptomyces; ZF0006087= Streptomyces; ZF0050446= Bacterium; ZF0050445= Bacterium; ZF0006086= Streptomyces; ZF0002322= Rhodococcus; ZF0003538= Actinomyces; ZF0003535= Actinomyces;

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 120  
 15 ggcgatcacg tcgtcctctc cttcattccc tcgtgtggac gctgccgttg gtgcgcagtc  
 180  
 ggacagagca acctctgcga cctcggcgcc attctgatgg ccggcgacaca ggtcgacggg  
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 20 acgtaaccgcg cgacagctcg cgggcacgac gtcgga  
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25 <211> 279  
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30 <220>  
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 40 gggcacgaag gagcgggggt ggtcgaggcc gtcggctcgt cgatcgacag cattgcgccc  
 120  
 ggtgatcacg tgttgctgag ctaccgcagt tcgggtgtgt gcaggcagtg cctcagcggg  
 180  
 45 catcgggctg actgcgaaag ctcacacggg ctcaacagct ctggcgacag caccgacggc  
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50 279  
 <210> 47

55 <211> 279  
 <212> DNA  
 <213> unknown

<220>

<221> source

5 <223> ZF0002333= Rhodococcus erythropolis

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120

ggatgatcacg tattgctgag ctaccgcagt tgcgggtgtat gcaggcaatg tctcagcgac  
15 180

catcgggcgt actgcgaaaag ctcacacggg ctcaacagct ctggcgcacg caccgacggc  
240

20 tgcagcgccg tccggcgaaa cggaactccg atacgggtcc  
279

<210> 48

25 <211> 360

<212> DNA

<213> unknown

30 <220>

<221> source

35 <223> ZF0051303= Bacterium; ZF0051337= Methylomonas; ZF0002862= Streptomyces clavuligerus; ZF0050292= Bacterium; ZF0051305= Bacterium; ZF0003513= Actinomyces; ZF0002351= Nonomuraea roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces; ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504= Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces; ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces aureomonopodiales; ZF0006089= Streptomyces; ZF0006106= Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces; ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532= Actinomyces; ZF0003548= Nocardiaform;

40

45 <400> 48

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50 cacctcgtcc tcgggcacga atcgctgggc cgagtacgca ccgcgcccga cggcagcgg  
120

ttcgccgccg gtgatctcgt cgtcgggatc gtgcgcaggc ccgatccggt gccgtgcggg  
180

55 gcgtgtgcgc acggtgagtt cgacatgtgc cgcaacggtg agtacgtcga gcgcgggatc  
240

aagcagatcg acgggtacgg gtcgacgtcg tgggtggtgg acgccgacta cacggtcaag  
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 roseoviolacea; ZF0003769= Actinomyces; ZF0002017= Streptomyces;  
 ZF0051306= Bacterium; ZF0002016= Streptomyces; ZF0003504=  
 Actinomyces; ZF0006073= Streptomyces; ZF0003770= Actinomyces;  
 25 ZF0002352= Actinoplanes italicus; ZF0002378= Streptomyces  
 aureomonopodiales; ZF0006089= Streptomyces; ZF0006106=  
 Streptomyces; ZF0051325= Bacterium; ZF0006108= Streptomyces;  
 ZF0002440= Streptomyces; ZF0051302= Bacterium; ZF0003532=  
 Actinomyces; ZF0003548= Nocardiaform;  
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 35 ccgctcacgc tcggccacga gttcgtcggc gaggtcgtcg agaccggccg cgacgtgacc  
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 gacatccagg tcggcgacct ggtcagcggc gagggccacc tgggtctgagg caagtgccgc  
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 40 aactgcctgg ccggccgccc tcacctgtgc cgcgcgaccg tcggcctcgg tgtcggccgt  
 240  
 45 gacggcgcct tcgccagata cgtggtgctg cccgcctcca acgtgtgggt gcaccgggtg  
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 421  
 55 <210> 50  
 <211> 414



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 ZF0050330= *Bacillus*, ZF0002852= *Rhodococcus*; ZF0050310=  
*Arthrobacter paraffineus*; ZF0002437= *Streptomyces*; ZF0003712=  
*Micromonospora*; ZF0003765= *Streptomyces*; ZF0002332=  
*Streptomyces diatsatochromogenes*; ZF0003768= *Actinomyces*;  
 15 ZF0002379= *Streptomyces coelestis*; ZF0002443= *Streptomyces*;  
 ZF0002442= *Streptomyces*; ZF0002436= *Streptomyces*; ZF0050994=  
*Bacterium*; ZF0050992= *Bacterium*; ZF0050442= *Bacterium*;  
 ZF0002049= *Streptomyces*; ZF0006069= *Streptomyces*; ZF0006075=  
*Streptomyces*; ZF0004724= *Nocardiaform*; ZF0002392= *Actinoplanes*  
 20 *nipponensis*; ZF0002356= *Actinoplanes brasiliensis*; ZF0003501=  
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 ZF0006092= *Streptomyces*; ZF0006090= *Streptomyces*; ZF0006084=  
*Streptomyces*; ZF0006068= *Streptomyces*; ZF0050284= *Rhodococcus*;  
 ZF0050028= *Agrobacterium tumefaciens*; ZF0003540= *Actinomyces*;  
 25 ZF0003528= *Actinomyces*; ZF0003529= *Actinomyces*;  
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 35 ggctgccatg gataccgggc caccggcggc tggcgctttg gcaacatcat cgatggcgcc  
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 40 300  
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 5 *Arthrobacter paraffineus*; ZF0002437= *Streptomyces*; ZF0003712=  
*Micromonospora*; ZF0003765= *Streptomyces*; ZF0002332=  
*Streptomyces diatsatochromogenes*; ZF0003768= *Actinomyces*;  
 ZF0002379= *Streptomyces coelestis*; ZF0002443= *Streptomyces*;  
 ZF0002442= *Streptomyces*; ZF0002436= *Streptomyces*; ZF0050994=  
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 10 ZF0002049= *Streptomyces*; ZF0006069= *Streptomyces*; ZF0006075=  
*Streptomyces*; ZF0004724= *Nocardiaform*; ZF0002392= *Actinoplanes*  
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*Actinomyces*; ZF0051322= Bacterium; ZF0006078= *Streptomyces*;  
 ZF0006092= *Streptomyces*; ZF0006090= *Streptomyces*; ZF0006084=  
*Streptomyces*; ZF0006068= *Streptomyces*; ZF0050284= *Rhodococcus*;  
 15 ZF0050028= *Agrobacterium tumefaciens*; ZF0003540= *Actinomyces*;  
 ZF0003528= *Actinomyces*; ZF0003529= *Actinomyces*;

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 25 ccggggcgatc gcgtgctcgt ctcgtgtgtc accgcatgcg gtacgtgccg gttctgccgc  
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 240  
 30 ggcacccagg ccgaactcgt ccgagttccg tacgccgaca attcgaccca ccgcatcccc  
 300  
 gacgggtgtga gcgacgagca gatgctcatg ctcgccgaca tcctgcccac ctctacgag  
 35 360  
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 40 gatcggcctc tt  
 432

45 <210> 52

<211> 220

<212> DNA

50 <213> unknown

<220>

<221> source

55 <223> ZF0050310= *Arthrobacter paraffineus*

<400> 52

cgtcgacgtc gtcgtcgaca acgcgggatt cggaacacac ggggcattcg tggacgaaga  
 60

tcacgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca  
120

5 cacattcccg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacagc  
180

gtcgttccag cccgacaccgg gcatggccgt ctactgcgct  
220

10

<210> 53

<211> 226

15 <212> DNA

<213> unknown

20 <220>

<221> source  
<223> ZF0050310= *Arthrobacter paraffineus*

25 <400> 53  
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60

tctcgagcgc gtcacgtccg agattcagct caacatcgcc acgctggtcg agctgacaca  
120

30 cacattcctg cccgaccttc tcaccggccg cggagcactg gtcaacatcg ccagcacagc  
180

35 gtcgttccag cccgacaccgg gcatggccgt ctactgcgcc accaag  
226

<210> 54

40 <211> 237

<212> DNA

45 <213> unknown

<220>

<221> source  
50 <223> ZF0003535= *Actinomyces*

<400> 54  
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60

55 acccccgcgc attttgagcg catcctgcgg gtgaacctga ccggcgtctt caacctgagc  
120

caagccgtca ttccttgat gattcagcgc ggccggaggaa gcatcgtctc gatttcctcg  
180

5 ctgtcggcgc agaacggcgg ggggatcttc ggcggcgccc actattgcgc aaccaag  
237

<210> 55

10 <211> 229

<212> DNA

<213> unknown

15 <220>

<221> source

20 <223> ZF0003535= Actinomyces

<400> 55  
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25 gccgctaaag gactggcaga ccatggtgaa caccaacatc accggtctac tgaacatcac  
120

ccaccatctc ctgccgacac tgatcgaccg taaaggatc gtcgtcaacc tttcgtctgt  
180

30 tgccgcgcac tatccctata cgggcggcaa tgtatactgc gcctccaag  
229

35 <210> 56

<211> 216

<212> DNA

40 <213> unknown

<220>

45 <221> source

<223> ZF0050310= Arthrobacter paraffineus

<400> 56  
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50 60

ggcgacatcg acgaagccac tctcgcgcga gcagccaagg atttgggcat ccgcacgttc  
120

55 gggcgccctcg acgtcaccga cccgcctcg ttcttcgact tcctcgacac cgtcgaaggt  
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gaactcggcc cgatcgacgt gctgatcaac aacgcg  
216

<210> 57  
5 <211> 225  
<212> DNA  
10 <213> unknown  
<220>  
<221> source  
15 <223> ZF0080310= *Arthrobacter paraffineus*  
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60  
20 ggcgacatca acgaaaccgt gggaaacggct gcggtcgccg aactcgggtgg agagtcggtc  
120  
gcccgtttcg cttcctgcga cgtgcgtgac tccggacagg tcgaggccat gctcgatctg  
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25 gccgaaagcg ctttcgggtcc agtcgatgtc atgatgaaca acgcg  
225  
30 <210> 58  
<211> 216  
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35 <213> unknown  
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40 <223> ZF0080310= *Arthrobacter paraffineus*  
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45 ggcgacatcg acgaggcacg tgctaaggag accgccgccg aactgggggt taaggttgtc  
120  
50 accgcctcg atgtcacca ccttgactcg ttcaaagact ttctcgacct agtcgagga  
180  
gacctcggcc ccctcgacgt gctgatcaac aacgcg  
216  
55 <210> 59  
<211> 222

<212> DNA

<213> unknown

5 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

10 <400> 59  
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60

15 gacatcaacg aaaccgtggg aacggctgcg gtcgccgaac tcggtggaga gtcggtcgcc  
120

cgtttcgctt cctgcgacgt gcgtgactcc ggacaggctc aggccatgct cgatctggcc  
180

20 gaaagecgtt tcggtccagt cgatgtcatc gtgaacaacg cg  
222

<210> 60

<211> 222

25 <212> DNA

<213> unknown

30 <220>

<221> source

<223> ZF0080310= *Arthrobacter paraffineus*

35 <400> 60  
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60

40 atcaacgaaa ccgtgggaac ggctgcggtc ggcgaactcg gtggagagtc ggtcgcccgt  
120

ttcgtttcct gcgacgtgcg tgactccgga caggctcagg ccatgctcga tctggccgaa  
180

45 agcgcttttcg gtccagtcga tgtcatggtc aacaacgccg gc  
222

<210> 61

50 <211> 186

<212> DNA

55 <213> unknown

<220>

<221> source

<223> ZF0002333= Rhodococcus erythropolis

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gaatcgcagt acggcacacc cgcgctcgcc cttgaggccg atgtgcgcga ccgcgcgcgc  
120  
10 gtgagcgccg ctttcgaagc caccgtcgcc gaatggggac gcttcgacta cctcgtcaac  
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aacgcc  
186  
15  
<210> 62  
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20  
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25  
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<400> 62  
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ctcgatcccg aacctgccgc tcagaccgag cgcgatatca aagccacagg tggacaggct  
120  
35 gtctcgtgcg tcggctccgt tgccgaggac gggttcgccg aacgcttcgt gaacactgcc  
180  
gtcgaatcat tcggcggact cgacgtcatg gtgaacaacg cg  
40 222  
<210> 63  
45  
<211> 231  
<212> DNA  
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50  
<220>  
<221> source  
<223> ZF0002333= Rhodococcus erythropolis  
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gtcgccaggc gggcagatcg cctcgaagcc ctgctaccg aactccgcgt cgccacggc  
120

5 atcacagtca cagttctgcc tgccgacctg gcggcgcccg ggcgcggcgc aacactgcac  
180

caggagctga caagccgtgg catcacgctc acctcgctga tcaacaacgc c  
231

10 <210> 64

<211> 216

15 <212> DNA

<213> unknown

<220>

20 <221> source

<223> ZF0003535= Actinomyces

<400> 64

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gtcgacatcg acgaggcacg tgcgaagggg gccgcgcgcg aactcggggt gaaggtcgtc  
120

30 acccgactcg acgtcaccga acctgactcg ttcaacaacgt ttctggacct ggtcgaacgt  
180

gaactcggac ccctcgacat cctgggtcaac aacgcg  
216

35 <210> 65

40 <211> 201

<212> DNA

<213> unknown

45 <220>

<221> source

50 <223> ZF0050310= Arthrobacter paraffineus

<400> 65

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55 gtcgcactta tcgaatcgca gtacggcaca cccgcgctcg cccttgaggc cgatgtgcgc  
120

gaccgcgccg ccgtgagcgc cgctttcgaa gccaccgctg ccgaatgggg acgcttcgac  
180



tacctcgtca acaacgccgg c  
201

5  
<210> 66  
<211> 201  
  
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10  
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60  
  
gtcgcactta tcgaatcgca gtacggcaca cccgcgctcg cccttgaggc cgatgtgcgc  
120  
  
25 gaccgcgccg ccgtgagcgc cgctttcgaa gccaccgtcg ccgaatgggg acgcttcgac  
180  
  
tacctcgtca acaacgccgg c  
201

30  
  
<210> 67  
  
<211> 1047  
35  
<212> DNA  
  
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40  
  
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<223> ZF0050310= *Arthrobacter paraffineus*  
  
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cccgagcccg gtccaggtga agtgctcctg gaagtcaccg ctgcccgcgt ctgccactcg  
50  
120  
  
gacgacttca tcatgagcct gcccgagag cagtacacct acggccttcc tctcacgctc  
180  
  
55 ggccacgaag gcgccggccg ggtcgccgcc gtcggcgagg gcgtcgaagg actcgacatc  
240  
  
ggaaccaatg tcgtcgtcta cggaccctgg ggctgtggca gctgttggca ctgctcgcaa  
300

ggactcgaaa actactgttc tcgggcaaaa gaactcggca tcaatcctcc tgggtctcgg  
 360

5 gcacccggcg cgttggecga attcatgac gtcgattcac ctcgccacct cgtcccgatc  
 420

ggcgacctcg atccgggtcaa gacgggtgcca ctgaccgacg ccgggtctgac tccgtatcac  
 480

10 gcgatcaagc gttcactgcc gaaacttcgc ggtggcgcggt acgccgtcgt catcgggtacc  
 540

15 ggcggtctcg gccatgtcgc catccaactc ctccgccacc tctcggcagc aaccgtcatc  
 600

gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg  
 660

20 gtcctgtccg acaaggacgc ggccgagAAC gtccgcagga tcaccggaag tcagggcgcc  
 720

gcactgggttc tcgacttcgt cggctatcag cccaccatcg acaccgcgat ggctgtcgcc  
 780

25 ggcgtcggat cggacgtcac gatcgtcggg atcggcgacg ggcaggccca tgccaaagtc  
 840

ggggttcttcc aaagtcctta cgaggcttct gtgacagttc cgtactgggg tgcccgaac  
 900

30 gagctgatcg aattgatcga cctggcgcac gccggcatct tcgacatcgc ggtggagacc  
 960

35 ttcagtctcg acaacggcgc cgaagcgtat cgacgactgg ccgccggaac gtcagcggc  
 1020

cgcgcgggttg tggtccttg tctgtag  
 1047

40 <210> 68

<211> 1047

45 <212> DNA

<213> unknown

<220>

50 <221> source

<223> ZF0050310= *Arthrobacter paraffineus*

<400> 68

55 atgaaggcaa tccagtacac gagaatcggc gcagaaccgc aactcacgga gattcccaaa  
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cccgagcccg gtccaggtga agtgctcctg gaagtcaccg ctgccggcgt ctgccactcg  
 120

gacgacttca tcatgagcct gccgaagag cagtacacct acggccttcc tctcacgctc  
180

5 ggccacgaag gcgccggccg ggtcgccgcc gtcggcgagg gcgtcgaagg actcgacatc  
240

ggaaccaatg tcgtcgtcta cggaccctgg ggctgtggca gctgttggca ctgctcgcaa  
300

10 ggactcgaaa actactgttc tcgggcaaaa gaactcggca tcaatcctcc tggctctcgg  
360

gcacccggcg cgttggccga attcatgac gtcgattcac ctgccacct cgtcccgatc  
420

15 ggcgacctcg atccgggtcaa gacggtgcca ctgaccgacg ccggtctgac tccgtatcac  
480

20 gcgatcaagc gttcactgcc gaaacttcgc ggtggcgcggt acgcgctcgt catcggtacc  
540  
ggcgggtctcg gccatgtcgc catccaactc ctccgccacc tctcggcagc aaccgtcatc  
600

25 gcactcgacg tgagcgcgga caagctcgaa ctggcaacca aggtaggcgc tcacgaagtg  
660

gtcctgtccg acaaggacgc ggccgagaac gtccgcagga tcaccggaag tcagggcgcc  
720

30 gcactgggttc tcgacttcgt cggctatcag ccaccatcg acaccgcgat ggctgtcgcc  
780

ggcgtcggat cggacgtcac gatcgtcggg atcggcgacg ggcaggccca tgccaaagtc  
840

35 gggttcttcc aaagtcctta cgaggcttct gtgacagttc cgtactgggg tgcccgcaac  
900

40 gagctgatcg aattgatcga cctggcgcac gccggcatct tcgacatcg ggtggagacc  
960

ttcagtctcg acaacggcgc cgaagcgtat cgacgactgg ccgccggaac gctcagcggc  
1020

45 cgcgcggttg tggcccttg tctgtag